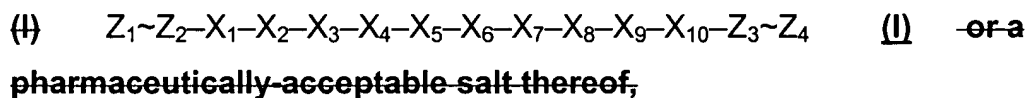


AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (currently amended): An isolated compound which inhibits pilus assembly, or a pharmaceutically-acceptable salt thereof, said compound comprising a mimic of a chaperone G1 beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 10 to 20 residue peptide, having an amino terminus and a carboxy terminus, according to formula (I):



wherein:

Z_1 is the amino terminus of the mimic peptide, Z_1 having the formula
R-C(O)-NR- or RRN-;

Z_2 is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z_1 to X_1 ;

X_1 is any amino acid residue;

X_2 is any amino acid residue;

X_3 is a hydrophobic residue or a hydroxyl-substituted aliphatic residue;

X_4 is any amino acid residue;

X_5 is a hydrophobic residue or Gly;

X_6 is a hydrophobic or a hydrophilic residue;

X_7 is Gly, an amide-substituted polar residue or a hydrophobic residue;

X_8 is an amino acid residue other than an aliphatic residue;

X_9 is an aliphatic residue;

X_{10} is any amino acid residue;

Z_3 is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or
(ii) a bond connecting Z_4 to X_{10} ;

Z_4 is the carboxy terminus of the peptide, Z_4 having the formula $-C(O)OR$ or $-C(O)NRR$;

each R is independently hydrogen, (C_1-C_6) alkyl, (C_2-C_6) alkenyl, (C_2-C_6) alkynyl or (C_6-C_{14}) aryl;

each "-" between residues X_1 through X_{10} , Z_2 and X_1 and X_{10} and Z_3 independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" represents a bond.

Claim 2-3 (cancelled)

Claim 4 (previously presented): The compound of claim 1 wherein the compound exhibits antibacterial activity against a Gram-negative bacterium.

Claim 5 (currently amended): An isolated compound which inhibits pilus assembly, said compound comprising SEQ ID NO: 1, wherein the compound is a mimic of a chaperone G_1 beta-strand and the compound exhibits antibacterial activity against a Gram-negative bacterium. The compound of claim 4 wherein said mimic comprises SEQ ID NO: 1 or an analog thereof.

Claim 6 (cancelled)

Claim 7 (cancelled)

Claim 8 (previously presented): The compound of claim 1 wherein the compound comprises a mimic of an amino terminal motif of a pilus subunit selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO:

22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 9 (currently amended): The compound of claim 8 wherein said mimic of an amino-terminal motif of a pilus subunit further comprises the amino acid sequence SDVAFRGNLL (SEQ ID NO: 12) ~~or an analog thereof~~.

Claim 10 (cancelled)

Claim 11 (cancelled)

Claim 12 (cancelled)

Claim 13 (previously presented): The compound of claim 1 wherein one or more of the following conditions are satisfied:

each "-" between residues X_1 through X_{10} , Z_2 and X_1 and X_{10} and Z_3 is an amide linkage;

Z_1 is H_2N- ;

Z_4 is $-C(O)OH$ or a salt thereof;

Z_2 is a bond connecting Z_1 to X_1 ;

Z_3 is a bond connecting Z_4 to X_{10} ;

X_1 is an amino acid residue other than a basic residue;

X_2 is an amino acid residue other than an aliphatic residue;

X_3 is an aliphatic residue or T;

X_4 is an amino acid residue other than an acidic residue;

X_5 is an aliphatic residue, F or G;

X_7 is G, N or A; or

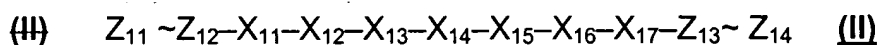
X_{10} is an aliphatic or a polar residue.

Claim 14 (previously presented): The compound of claim 13 wherein the mimic comprises a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID

NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28 and SEQ ID NO: 29.

Claim 15 (cancelled)

Claim 16 (currently amended): An isolated compound which inhibits pilus assembly, or a pharmaceutically-acceptable salt thereof, the compound comprising a mimic of a chaperone G₁ beta-strand or a mimic of an amino terminal motif of a pilus subunit, wherein the mimic is a 7 to 17 residue peptide ~~or peptide analog~~, having an amino terminus and a carboxy terminus, according to formula (II):



~~or a pharmaceutically-acceptable salt thereof,~~

wherein:

Z₁₁ is the amino terminus of the peptide, Z₁₁ having the formula R'-C(O)-NR'- or R'R'N-;

Z₁₂ is (i) a first peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z₁₁ to X₁₁;

X₁₁ is any amino acid residue;

X₁₂ is any amino acid residue;

X₁₃ is a hydrophobic residue;

X₁₄ is any amino acid residue;

X₁₅ is a hydrophobic residue;

X₁₆ is any amino acid residue;

X₁₇ is hydrophobic residue or a hydroxyl-substituted aliphatic residue;

Z₁₃ is (i) a second peptide sequence consisting of 1 to 5 amino acid residues or (ii) a bond connecting Z₁₄ to X₁₇;

Z₁₄ is the carboxy terminus of the peptide, Z₁₄ having the formula -C(O)OR' or -C(O)NR'R';

each R' is independently hydrogen, (C₁-C₆) alkyl, (C₂-C₆) alkenyl, (C₂-C₆) alkynyl or (C₆-C₁₄) aryl;

each "-" between residues X₁₁ through X₁₇, Z₁₂ and X₁₁ and X₁₇ and Z₁₃ independently represents an amide linkage, a substituted amide linkage or an isostere of an amide linkage; and

each "~" independently represents a bond.

Claim 17 (previously presented): The compound of claim 16 wherein one or more of the following conditions are satisfied:

each "-" between residues X₁₁ through X₁₇, Z₁₂ and X₁₁ and X₁₇ and Z₁₃ is an amide linkage;

Z₁₁ is H₂N-;

Z₁₄ is -C(O)OH or a salt thereof;

Z₁₂ is a bond connecting Z₁₁ to X₁₁;

Z₁₃ is a bond connecting Z₁₄ to X₁₇;

X₁₁ is an amino acid residue other than a basic residue;

X₁₃ is an aliphatic residue or M;

X₁₄ is an amino acid residue other than an aromatic residue;

X₁₅ is an aliphatic residue, F or M; and

X₁₇ is an aliphatic residue, F, M or a hydroxyl-substituted aliphatic residue.

Claim 18 (cancelled)

Claim 19 (currently amended): The compound of any one of claims 1, 2, 5, 8, 9, 13, 14, 16, or 17 wherein said compound exhibits antibacterial activity against one or more Gram-negative bacterium selected from the group consisting of *E. coli*, *H. influenzae*, *S. euteriditis*, *S. typhimurium*, *B. pertussis*, *Y. pestis*, *Y. enterocolitica*, *H. pylori* and *K. pneumoniae*.

Claims 20-135 (cancelled)

Claim 136 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting of SEQ ID NO: 12.

Claim 137 (previously presented): An isolated compound which inhibits pilus assembly, the compound consisting essentially of SEQ ID NO: 12, wherein the compound is a mimic of an amino terminal motif of a pilus subunit.

Claim 138 (previously presented): An isolated compound which inhibits pilus assembly, the compound comprising a mimic of an amino terminal motif of a pilus subunit, wherein the mimic comprises SEQ ID NO:12.

Claim 139 (previously presented): The compound of claim 138 wherein the compound competitively binds to a pilus subunit hydrophobic groove.

Claim 140-158 (cancelled)

Claim 159 (**new**) The compound of claim 1 wherein the compound consists essentially of a 10 to 20 residue peptide according to formula (I).

Claim 160 (**new**) The compound of claim 16 wherein the compound consists essentially of a 7 to 17 residue peptide according to formula (II).